

(1) GENERAL INFORMATION:

(i) APPLICANT:

(B) NAME: CREATIVE BIOMOLCULES, INC

(C) STREET: 45 SOUTH STREET

(D) STATE: HOPKINTON

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 01748

(G) TELEPHONE: (508)-435-9001

(H) TELEFAX: (508)-435-0992

(I) TELEX:

(i) APPLICANT:

APPLICANT:
(B) NAME: LUDWIG INSTITUTE FOR CANCER RESEARCH
OF THE AMERICAS

(C) STREET: 1345 AVENUE OF THE AMERICAS

(D) STATE: NY

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 10105

(G) TELEPHONE: (212)-765-3000

(H) TELEFAX:

(I) TELEEX:

(ii) TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
THIBEAULT

(B) STREET: 53 STATE STREET

(C) CITY: BOSTON

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: PITCHER, EDMUND R.

(B) REGISTRATION NUMBER: 27,829

(C) REFERENCE/DOCKET NUMBER: CRP-097PC

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 248-7000

(B) TELEFAX: (617) 248-7100

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1509
- (D) OTHER INFORMATION: /product= "Human ALK1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|----|---|-----|
| 20 | ATG ACC TTG GGC TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC | 48 |
| | Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala | |
| | 1 5 10 15 | |
| 25 | TTG GTG ACC CAG GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG | 96 |
| | Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val | |
| | 20 25 30 | |
| 30 | ACC TGC ACG TGT GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG | 144 |
| | Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly | |
| | 35 40 45 | |
| 35 | GCC TGG TGC ACA GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG | 192 |
| | Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln | |
| | 50 55 60 | |
| 40 | GAA CAT CGG GGC TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC | 240 |
| | Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg | |
| | 65 70 75 80 | |
| 45 | CCC ACC GAG TTC GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC | 288 |
| | Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn | |
| | 85 90 95 | |
| 50 | CAC AAC GTG TCC CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG | 336 |
| | His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln | |
| | 100 105 110 | |
| 55 | CCG GGA ACA GAT GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC | 384 |
| | Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala | |
| | 115 120 125 | |
| 60 | TTG CTG GCC CTG GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA | 432 |
| | Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg | |
| | 130 135 140 | |
| 65 | CGG AGG CAG GAG AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC | 480 |
| | Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser | |
| | 145 150 155 160 | |
| 70 | AGT CTC ATC CTG AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC | 528 |

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| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Ser | Leu | Ile | Leu | Lys | Ala | Ser | Glu | Gln | Gly | Asp | Thr | Met | Leu | Gly | Asp | |
| | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 5 | CTC | CTG | GAC | AGT | GAC | TGC | ACC | ACA | GGG | AGT | GGC | TCA | GGG | CTC | CCC | TTC | 576 |
| | Leu | Leu | Asp | Ser | Asp | Cys | Thr | Thr | Gly | Ser | Gly | Ser | Gly | Leu | Pro | Phe | |
| | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 10 | CTG | GTG | CAG | AGG | ACA | GTG | GCA | CGG | CAG | GTT | GCC | TTG | GTG | GAG | TGT | GTG | 624 |
| | Leu | Val | Gln | Arg | Thr | Val | Ala | Arg | Gln | Val | Ala | Leu | Val | Glu | Cys | Val | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 15 | GGA | AAA | GGC | CGC | TAT | GGC | GAA | GTG | TGG | CGG | GGC | TTG | TGG | CAC | GGT | GAG | 672 |
| | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Arg | Gly | Leu | Trp | His | Gly | Glu | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| 20 | AGT | GTG | GCC | GTC | AAG | ATC | TTC | TCC | TCG | AGG | GAT | GAA | CAG | TCC | TGG | TTC | 720 |
| | Ser | Val | Ala | Val | Lys | Ile | Phe | Ser | Ser | Arg | Asp | Glu | Gln | Ser | Trp | Phe | |
| | | | | | | 230 | | | | | 235 | | | | | 240 | |
| 25 | CGG | GAG | ACT | GAG | ATC | TAT | AAC | ACA | GTA | TTG | CTC | AGA | CAC | GAC | AAC | ATC | 768 |
| | Arg | Glu | Thr | Glu | Ile | Tyr | Asn | Thr | Val | Leu | Leu | Arg | His | Asp | Asn | Ile | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| 30 | CTA | GGC | TTC | ATC | GCC | TCA | GAC | ATG | ACC | TCC | CGC | AAC | TCG | AGC | ACG | CAG | 816 |
| | Leu | Gly | Phe | Ile | Ala | Ser | Asp | Met | Thr | Ser | Arg | Asn | Ser | Ser | Thr | Gln | |
| | | | | 260 | | | | | 265 | | | | | 270 | | | |
| 35 | CTG | TGG | CTC | ATC | ACG | CAC | TAC | CAC | GAG | CAC | GGC | TCC | CTC | TAC | GAC | TTT | 864 |
| | Leu | Trp | Leu | Ile | Thr | His | Tyr | His | Glu | His | Gly | Ser | Leu | Tyr | Asp | Phe | |
| | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 40 | CTG | CAG | AGA | CAG | ACG | CTG | GAG | CCC | CAT | CTG | GCT | CTG | AGG | CTA | GCT | GTG | 912 |
| | Leu | Gln | Arg | Gln | Thr | Leu | Glu | Pro | His | Leu | Ala | Leu | Arg | Leu | Ala | Val | |
| | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 45 | TCC | GCG | GCA | TGC | GGC | CTG | GCG | CAC | CTG | CAC | GTG | GAG | ATC | TTC | GGT | ACA | 960 |
| | Ser | Ala | Ala | Cys | Gly | Leu | Ala | His | Leu | His | Val | Glu | Ile | Phe | Gly | Thr | |
| | | | | | 310 | | | | | | 315 | | | | | 320 | |
| 50 | CAG | GGC | AAA | CCA | GCC | ATT | GCC | CAC | CGC | GAC | TTC | AAG | AGC | CGC | AAT | GTG | 1008 |
| | Gln | Gly | Lys | Pro | Ala | Ile | Ala | His | Arg | Asp | Phe | Lys | Ser | Arg | Asn | Val | |
| | | | | | 325 | | | | | 330 | | | | | 335 | | |
| 55 | CTG | GTC | AAG | AGC | AAC | CTG | CAG | TGT | TGC | ATC | GCC | GAC | CTG | GGC | CTG | GCT | 1056 |
| | Leu | Val | Lys | Ser | Asn | Leu | Gln | Cys | Cys | Ile | Ala | Asp | Leu | Gly | Leu | Ala | |
| | | | | 340 | | | | | 345 | | | | | 350 | | | |
| 60 | GTG | ATG | CAC | TCA | CAG | GGC | AGC | GAT | TAC | CTG | GAC | ATC | GGC | AAC | AAC | CCG | 1104 |
| | Val | Met | His | Ser | Gln | Gly | Ser | Asp | Tyr | Leu | Asp | Ile | Gly | Asn | Asn | Pro | |
| | | | 355 | | | | | 360 | | | | | 365 | | | | |
| 65 | AGA | GTG | GGC | ACC | AAG | CGG | TAC | ATG | GCA | CCC | GAG | GTG | CTG | GAC | GAG | CAG | 1152 |
| | Arg | Val | Gly | Thr | Lys | Arg | Tyr | Met | Ala | Pro | Glu | Val | Leu | Asp | Glu | Gln | |
| | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 70 | ATC | CGC | ACG | GAC | TGC | TTT | GAG | TCC | TAC | AAG | TGG | ACT | GAC | ATC | TGG | GCC | 1200 |
| | Ile | Arg | Thr | Asp | Cys | Phe | Glu | Ser | Tyr | Lys | Trp | Thr | Asp | Ile | Trp | Ala | |
| | | | | | 385 | | 390 | | | | 395 | | | | | 400 | |
| 75 | TTT | GGC | CTG | GTG | CTG | TGG | GAG | ATT | GCC | CGC | CGG | ACC | ATC | GTG | AAT | GGC | 1248 |

5 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
 405 410 415 1296
 ATC GTG GAG GAC TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC
 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
 420 425 430
 10 CCC AGC TTT GAG GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC
 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
 435 440 445 1344
 CCC ACC ATC CCT AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA
 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
 450 455 460 1392
 15 GCT CAG ATG ATG CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC
 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
 465 470 475 1440
 20 ACC GCG CTG CGG ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
 485 490 495 1488
 25 GAG AAG CCT AAA GTG ATT CAA
 Glu Lys Pro Lys Val Ile Gln 1509
 500

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 503 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
 1 5 10 15
 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
 20 25 30
 45 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
 35 40 45
 50 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
 50 55 60
 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
 65 70 75 80
 55 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
 85 90 95
 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
 100 105 110

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Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
115 120 125

5 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
130 135 140

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
145 150 155 160

10 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
165 170 175

Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
180 185 190

15 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
195 200 205

20 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
210 215 220

Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
225 230 235 240

25 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
245 250 255

Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
260 265 270

30 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
275 280 285

35 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
290 295 300

Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
305 310 315 320

40 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
325 330 335

Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
340 345 350

45 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
355 360 365

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
370 375 380

Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
385 390 395 400

55 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
405 410 415

Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
420 425 430

60

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Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
435 440 445

Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
450 455 460

Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
465 470 475 480

Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
485 490 495

Glu Lys Pro Lys Val Ile Gln
500

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 104..1633
(D) OTHER INFORMATION: /product= "Human ALK2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG 60

GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA 115
Met Val Asp Gly
1

GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT 163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
5 10 15 20

ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG 211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
25 30 35

TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG 259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
40 45 50

TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA 307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
55 60 65

GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG 355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
70 75 80

60

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|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | CCG | TCC | CCT | GGC | CAA | GCT | GTG | GAG | TGC | TGC | CAA | GGG | GAC | TGG | TGT | AAC | 403 |
| | Pro | Ser | Pro | Gly | Gln | Ala | Val | Glu | Cys | Cys | Gln | Gly | Asp | Trp | Cys | Asn | 100 |
| | 85 | | | | | 90 | | | | | 95 | | | | | | |
| 5 | AGG | AAC | ATC | ACG | GCC | CAG | CTG | CCC | ACT | AAA | GGA | AAA | TCC | TTC | CCT | GGA | 451 |
| | Arg | Asn | Ile | Thr | Ala | Gln | Leu | Pro | Thr | Lys | Gly | Lys | Ser | Phe | Pro | Gly | 115 |
| | | | | | 105 | | | | | 110 | | | | | | | |
| 10 | ACA | CAG | AAT | TTC | CAC | TTG | GAG | GTT | GGC | CTC | ATT | ATT | CTC | TCT | GTA | GTG | 499 |
| | Thr | Gln | Asn | Phe | His | Leu | Glu | Val | Gly | Leu | Ile | Ile | Leu | Ser | Val | Val | |
| | | | | | 120 | | | | 125 | | | | | 130 | | | |
| 15 | TTC | GCA | GTA | TGT | CTT | TTA | GCC | TGC | CTG | CTG | GGA | GTT | GCT | CTC | CGA | AAA | 547 |
| | Phe | Ala | Val | Cys | Leu | Leu | Ala | Cys | Leu | Leu | Gly | Val | Ala | Leu | Arg | Lys | |
| | | | | | 135 | | | 140 | | | | | | 145 | | | |
| 20 | TTT | AAA | AGG | CGC | AAC | CAA | GAA | CGC | CTC | AAT | CCC | CGA | GAC | GTG | GAG | TAT | 595 |
| | Phe | Lys | Arg | Arg | Asn | Gln | Glu | Arg | Leu | Asn | Pro | Arg | Asp | Val | Glu | Tyr | |
| | | 150 | | | | | 155 | | | | | 160 | | | | | |
| 25 | GGC | ACT | ATC | GAA | GGG | CTC | ATC | ACC | ACC | AAT | GTT | GGA | GAC | AGC | ACT | TTA | 643 |
| | Gly | Thr | Ile | Glu | Gly | Leu | Ile | Thr | Thr | Asn | Val | Gly | Asp | Ser | Thr | Leu | |
| | | | | | | 170 | | | | | 175 | | | | | 180 | |
| 30 | GCA | GAT | TTA | TTG | GAT | CAT | TCG | TGT | ACA | TCA | GGA | AGT | GGC | TCT | GGT | CTT | 691 |
| | Ala | Asp | Leu | Leu | Asp | His | Ser | Cys | Thr | Ser | Gly | Ser | Gly | Ser | Gly | Leu | |
| | | | | | 185 | | | | | 190 | | | | | 195 | | |
| 35 | CCT | TTT | CTG | GTA | CAA | AGA | ACA | GTG | GCT | CGC | CAG | ATT | ACA | CTG | TTG | GAG | 739 |
| | Pro | Phe | Leu | Val | Gln | Arg | Thr | Val | Ala | Arg | Gln | Ile | Thr | Leu | Leu | Glu | |
| | | | | | 200 | | | | 205 | | | | | 210 | | | |
| 40 | TGT | GTC | GGG | AAA | GGC | AGG | TAT | GGT | GAG | GTG | TGG | AGG | GGC | AGC | TGG | CAA | 787 |
| | Cys | Val | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Arg | Gly | Ser | Trp | Gln | |
| | | | | | 215 | | | 220 | | | | | 225 | | | | |
| 45 | GGG | GAA | AAT | GTT | GCC | GTG | AAG | ATC | TTC | TCC | TCC | CGT | GAT | GAG | AAG | TCA | 835 |
| | Gly | Glu | Asn | Val | Ala | Val | Lys | Ile | Phe | Ser | Ser | Arg | Asp | Glu | Lys | Ser | |
| | | | | | | | 235 | | | | | 240 | | | | | |
| 50 | TGG | TTC | AGG | GAA | ACG | GAA | TTG | TAC | AAC | ACT | GTG | ATG | CTG | AGG | CAT | GAA | 883 |
| | Trp | Phe | Arg | Glu | Thr | Glu | Leu | Tyr | Asn | Thr | Val | Met | Leu | Arg | His | Glu | |
| | | | | | | 250 | | | | | 255 | | | | | 260 | |
| 55 | AAT | ATC | TTA | GGT | TTC | ATT | GCT | TCA | GAC | ATG | ACA | TCA | AGA | CAC | TCC | AGT | 931 |
| | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ser | Asp | Met | Thr | Ser | Arg | His | Ser | Ser | |
| | | | | | 265 | | | | | 270 | | | | | 275 | | |
| 60 | ACC | CAG | CTG | TGG | TTA | ATT | ACA | CAT | TAT | CAT | GAA | ATG | GGA | TCG | TTG | TAC | 979 |
| | Thr | Gln | Leu | Trp | Leu | Ile | Thr | His | Tyr | His | Glu | Met | Gly | Ser | Leu | Tyr | |
| | | | | | 280 | | | | 285 | | | | | 290 | | | |
| 65 | GAC | TAT | CTT | CAG | CTT | ACT | ACT | CTG | GAT | ACA | GTT | AGC | TGC | CTT | CGA | ATA | 1027 |
| | Asp | Tyr | Leu | Gln | Leu | Thr | Thr | Leu | Asp | Thr | Val | Ser | Cys | Leu | Arg | Ile | |
| | | | | | 295 | | | 300 | | | | | 305 | | | | |
| 70 | GTG | CTG | TCC | ATA | GCT | AGT | GGT | CTT | GCA | CAT | TTG | CAC | ATA | GAG | ATA | TTT | 1075 |
| | Val | Leu | Ser | Ile | Ala | Ser | Gly | Leu | Ala | His | Leu | His | Ile | Glu | Ile | Phe | |
| | | | | | | | 315 | | | | | 320 | | | | | |

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| | | |
|----|---|------|
| | GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA | 1123 |
| | Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys | |
| | 325 330 335 340 | |
| 5 | AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC | 1171 |
| | Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly | |
| | 345 350 355 | |
| 10 | CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC | 1219 |
| | Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn | |
| | 360 365 370 | |
| 15 | AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT | 1267 |
| | Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp | |
| | 375 380 385 | |
| 20 | GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT | 1315 |
| | Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile | |
| | 390 395 400 | |
| 25 | TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC | 1363 |
| | Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser | |
| | 405 410 415 420 | |
| 30 | AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC | 1411 |
| | Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro | |
| | 425 430 435 | |
| 35 | AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA | 1459 |
| | Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln | |
| | 440 445 450 | |
| 40 | CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC | 1507 |
| | Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr | |
| | 455 460 465 | |
| 45 | TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA | 1555 |
| | Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala | |
| | 470 475 480 | |
| 50 | AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT | 1603 |
| | Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn | |
| | 485 490 495 500 | |
| 55 | TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTC | 1650 |
| | Ser Leu Asp Lys Leu Lys Thr Asp Cys | |
| | 505 510 | |
| 60 | GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT | 1710 |
| | TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC | 1770 |
| | GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA | 1830 |
| | ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA | 1890 |
| | AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG | 1950 |
| | GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT | 2010 |

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GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTCTTT ATTGCACTAG GAATTCTTTG 2070
 CATTCCCTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT 2130
 5 GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA 2190
 TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG 2250
 10 AATTGTTTAT ACACAACCTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTACAA 2310
 AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA 2370
 ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT 2430
 15 TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACTT TTTTTCAGTT CATATGCAGA 2490
 ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA 2550
 20 TTTCACTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC 2610
 ATTACGTGCA TTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTAAAT CTACTTTTTG 2670
 TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTC AAGTCAAAAA AAAA 2724
 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Asp Gly Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu
 1 5 10 15
 40 Pro Ser Pro Ser Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu
 20 25 30
 45 Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
 35 40 45
 Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
 50 55 60
 50 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
 65 70 75 80
 Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
 85 90 95
 55 Asp Trp Cys Asn Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys
 100 105 110
 60 Ser Phe Pro Gly Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile
 115 120 125

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090254 "101301"

| | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Leu | Ser | Val | Val | Phe | Ala | Val | Cys | Leu | Leu | Ala | Cys | Leu | Leu | Gly | Val |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| 5 | Ala | Leu | Arg | Lys | Phe | Lys | Arg | Arg | Asn | Gln | Glu | Arg | Leu | Asn | Pro | Arg |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| | Asp | Val | Glu | Tyr | Gly | Thr | Ile | Glu | Gly | Leu | Ile | Thr | Thr | Asn | Val | Gly |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| 10 | Asp | Ser | Thr | Leu | Ala | Asp | Leu | Leu | Asp | His | Ser | Cys | Thr | Ser | Gly | Ser |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| | Gly | Ser | Gly | Leu | Pro | Phe | Leu | Val | Gln | Arg | Thr | Val | Ala | Arg | Gln | Ile |
| 15 | | | 195 | | | | | 200 | | | | | 205 | | | |
| | Thr | Leu | Leu | Glu | Cys | Val | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Arg |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| 20 | Gly | Ser | Trp | Gln | Gly | Glu | Asn | Val | Ala | Val | Lys | Ile | Phe | Ser | Ser | Arg |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| | Asp | Glu | Lys | Ser | Trp | Phe | Arg | Glu | Thr | Glu | Leu | Tyr | Asn | Thr | Val | Met |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| 25 | Leu | Arg | His | Glu | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ser | Asp | Met | Thr | Ser |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| | Arg | His | Ser | Ser | Thr | Gln | Leu | Trp | Leu | Ile | Thr | His | Tyr | His | Glu | Met |
| 30 | | | 275 | | | | | 280 | | | | | 285 | | | |
| | Gly | Ser | Leu | Tyr | Asp | Tyr | Leu | Gln | Leu | Thr | Thr | Leu | Asp | Thr | Val | Ser |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| 35 | Cys | Leu | Arg | Ile | Val | Leu | Ser | Ile | Ala | Ser | Gly | Leu | Ala | His | Leu | His |
| | 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| | Ile | Glu | Ile | Phe | Gly | Thr | Gln | Gly | Lys | Pro | Ala | Ile | Ala | His | Arg | Asp |
| | | | | | 325 | | | | | 330 | | | | | 335 | |
| 40 | Leu | Lys | Ser | Lys | Asn | Ile | Leu | Val | Lys | Lys | Asn | Gly | Gln | Cys | Cys | Ile |
| | | | | 340 | | | | | 345 | | | | | 350 | | |
| | Ala | Asp | Leu | Gly | Leu | Ala | Val | Met | His | Ser | Gln | Ser | Thr | Asn | Gln | Leu |
| 45 | | | 355 | | | | | 360 | | | | | 365 | | | |
| | Asp | Val | Gly | Asn | Asn | Pro | Arg | Val | Gly | Thr | Lys | Arg | Tyr | Met | Ala | Pro |
| | | | 370 | | | | 375 | | | | | 380 | | | | |
| 50 | Glu | Val | Leu | Asp | Glu | Thr | Ile | Gln | Val | Asp | Cys | Phe | Asp | Ser | Tyr | Lys |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Arg | Val | Asp | Ile | Trp | Ala | Phe | Gly | Leu | Val | Leu | Trp | Glu | Val | Ala | Arg |
| | | | | | 405 | | | | | 410 | | | | | 415 | |
| 55 | Arg | Met | Val | Ser | Asn | Gly | Ile | Val | Glu | Asp | Tyr | Lys | Pro | Pro | Phe | Tyr |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| | Asp | Val | Val | Pro | Asn | Asp | Pro | Ser | Phe | Glu | Asp | Met | Arg | Lys | Val | Val |
| 60 | | | 435 | | | | | 440 | | | | | 445 | | | |

Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
 450 455 460
 5 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
 465 470 475 480
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr
 485 490 495
 10 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys
 500 505

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2932 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 310..1908
 (D) OTHER INFORMATION: /product= "Human ALK3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT 60
 35 CAGTTTAATA CTGTCTTGA ATTCTGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA 120
 AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG 180
 40 TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA 240
 TTAAATTTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC 300
 AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC 348
 45 Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala
 1 5 10
 TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG 396
 50 Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met
 15 20 25
 CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA 444
 Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu
 30 35 40 45
 55 AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC 492
 Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys
 50 55 60
 60 TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA 540

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| | Tyr | Cys | Ser | Gly | His | Cys | Pro | Asp | Asp | Ala | Ile | Asn | Asn | Thr | Cys | Ile | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | | | | 65 | | | | | 70 | | | | | | | 75 | |
| 5 | ACT | AAT | GGA | CAT | TGC | TTT | GCC | ATC | ATA | GAA | GAA | GAT | GAC | CAG | GGA | GAA | 588 |
| | Thr | Asn | Gly | His | Cys | Phe | Ala | Ile | Ile | Glu | Glu | Asp | Asp | Gln | Gly | Glu | |
| | | | 80 | | | | | 85 | | | | | 90 | | | | |
| 10 | ACC | ACA | TTA | GCT | TCA | GGG | TGT | ATG | AAA | TAT | GAA | GGA | TCT | GAT | TTT | CAG | 636 |
| | Thr | Thr | Leu | Ala | Ser | Gly | Cys | Met | Lys | Tyr | Glu | Gly | Ser | Asp | Phe | Gln | |
| | | | 95 | | | | 100 | | | | | 105 | | | | | |
| 15 | TGC | AAA | GAT | TCT | CCA | AAA | GCC | CAG | CTA | CGC | CGG | ACA | ATA | GAA | TGT | TGT | 684 |
| | Cys | Lys | Asp | Ser | Pro | Lys | Ala | Gln | Leu | Arg | Arg | Thr | Ile | Glu | Cys | Cys | |
| | 110 | | | | | 115 | | | | | 120 | | | | 125 | | |
| 20 | CGG | ACC | AAT | TTA | TGT | AAC | CAG | TAT | TTG | CAA | CCC | ACA | CTG | CCC | CCT | GTT | 732 |
| | Arg | Thr | Asn | Leu | Cys | Asn | Gln | Tyr | Leu | Gln | Pro | Thr | Leu | Pro | Pro | Val | |
| | | | | | 130 | | | | | 135 | | | | | 140 | | |
| 25 | GTC | ATA | GGT | CCG | TTT | TTT | GAT | GGC | AGC | ATT | CGA | TGG | CTG | GTT | TTG | CTC | 780 |
| | Val | Ile | Gly | Pro | Phe | Phe | Asp | Gly | Ser | Ile | Arg | Trp | Leu | Val | Leu | Leu | |
| | | | | 145 | | | | | 150 | | | | | 155 | | | |
| 30 | ATT | TCT | ATG | GCT | GTC | TGC | ATA | ATT | GCT | ATG | ATC | ATC | TTC | TCC | AGC | TGC | 828 |
| | Ile | Ser | Met | Ala | Val | Cys | Ile | Ile | Ala | Met | Ile | Ile | Phe | Ser | Ser | Cys | |
| | | | 160 | | | | | 165 | | | | | 170 | | | | |
| 35 | TTT | TGT | TAC | AAA | CAT | TAT | TGC | AAG | AGC | ATC | TCA | AGC | AGA | CGT | CGT | TAC | 876 |
| | Phe | Cys | Tyr | Lys | His | Tyr | Cys | Lys | Ser | Ile | Ser | Ser | Arg | Arg | Arg | Tyr | |
| | | | 175 | | | | 180 | | | | | 185 | | | | | |
| 40 | AAT | CGT | GAT | TTG | GAA | CAG | GAT | GAA | GCA | TTT | ATT | CCA | GTT | GGA | GAA | TCA | 924 |
| | Asn | Arg | Asp | Leu | Glu | Gln | Asp | Glu | Ala | Phe | Ile | Pro | Val | Gly | Glu | Ser | |
| | 190 | | | | | 195 | | | | | 200 | | | | 205 | | |
| 45 | CTA | AAA | GAC | CTT | ATT | GAC | CAG | TCA | CAA | AGT | TCT | GGT | AGT | GGG | TCT | GGA | 972 |
| | Leu | Lys | Asp | Leu | Ile | Asp | Gln | Ser | Gln | Ser | Ser | Gly | Ser | Gly | Ser | Gly | |
| | | | | | 210 | | | | | 215 | | | | | 220 | | |
| 50 | CTA | CCT | TTA | TTG | GTT | CAG | CGA | ACT | ATT | GCC | AAA | CAG | ATT | CAG | ATG | GTC | 1020 |
| | Leu | Pro | Leu | Leu | Val | Gln | Arg | Thr | Ile | Ala | Lys | Gln | Ile | Gln | Met | Val | |
| | | | | 225 | | | | | 230 | | | | | 235 | | | |
| 55 | CGG | CAA | GTT | GGT | AAA | GGC | CGA | TAT | GGA | GAA | GTA | TGG | ATG | GGC | AAA | TGG | 1068 |
| | Arg | Gln | Val | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Met | Gly | Lys | Trp | |
| | | | 240 | | | | 245 | | | | | | 250 | | | | |
| 60 | CGT | GGC | GAA | AAA | GTG | GCG | GTG | AAA | GTA | TTC | TTT | ACC | ACT | GAA | GAA | GCC | 1116 |
| | Arg | Gly | Glu | Lys | Val | Ala | Val | Lys | Val | Phe | Phe | Thr | Thr | Glu | Glu | Ala | |
| | | | 255 | | | | 260 | | | | | 265 | | | | | |
| 65 | AGC | TGG | TTT | CGA | GAA | ACA | GAA | ATC | TAC | CAA | ACT | GTG | CTA | ATG | CGC | CAT | 1164 |
| | Ser | Trp | Phe | Arg | Glu | Thr | Glu | Ile | Tyr | Gln | Thr | Val | Leu | Met | Arg | His | |
| | | | | | 275 | | | | | | 280 | | | | 285 | | |
| 70 | GAA | AAC | ATA | CTT | GGT | TTC | ATA | GCG | GCA | GAC | ATT | AAA | GGT | ACA | GGT | TCC | 1212 |
| | Glu | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ala | Asp | Ile | Lys | Gly | Thr | Gly | Ser | |
| | | | | | 290 | | | | | 295 | | | | | 300 | | |
| 75 | TGG | ACT | CAG | CTC | TAT | TTG | ATT | ACT | GAT | TAC | CAT | GAA | AAT | GGA | TCT | CTC | 1260 |

| | | | | | | | | | | | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|------------|------------|-----------|-----|-----|-----|-----|-----|-----|------|
| | Trp | Thr | Gln | Leu | Tyr | Leu | Ile | Thr | Asp | Tyr | His | Glu | Asn | Gly | Ser | Leu | |
| | | | | 305 | | | | | 310 | | | | | | | | 315 |
| 5 | TAT | GAC | TTC | CTG | AAA | TGT | GCT | ACA | CTG | GAC | ACC | AGA | GCC | CTG | CTT | AAA | 1308 |
| | Tyr | Asp | Phe | Leu | Lys | Cys | Ala | Thr | Leu | Asp | Thr | Arg | Ala | Leu | Leu | Lys | |
| | | | 320 | | | | | 325 | | | | | 330 | | | | |
| 10 | TTG | GCT | TAT | TCA | GCT | GCC | TGT | GGT | CTG | TGC | CAC | CTG | CAC | ACA | GAA | ATT | 1356 |
| | Leu | Ala | Tyr | Ser | Ala | Ala | Cys | Gly | Leu | Cys | His | Leu | His | Thr | Glu | Ile | |
| | | 335 | | | | | 340 | | | | | 345 | | | | | |
| 15 | TAT | GGC | ACC | CAA | GGA | AAG | CCC | GCA | ATT | GCT | CAT | CGA | GAC | CTA | AAG | AGC | 1404 |
| | Tyr | Gly | Thr | Gln | Gly | Lys | Pro | Ala | Ile | Ala | His | Arg | Asp | Leu | Lys | Ser | |
| | | 350 | | | | 355 | | | | | 360 | | | | | 365 | |
| 20 | AAA | AAC | ATC | CTC | ATC | AAG | AAA | AAT | GGG | AGT | TGC | TGC | ATT | GCT | GAC | CTG | 1452 |
| | Lys | Asn | Ile | Leu | Ile | Lys | Lys | Asn | Gly | Ser | Cys | Cys | Ile | Ala | Asp | Leu | |
| | | | | | 370 | | | | | 375 | | | | | 380 | | |
| 25 | GGC | CTT | GCT | GTT | AAA | TTC | AAC | AGT | GAC | ACA | AAT | GAA | GTT | GAT | GTG | CCC | 1500 |
| | Gly | Leu | Ala | Val | Lys | Phe | Asn | Ser | Asp | Thr | Asn | Glu | Val | Asp | Val | Pro | |
| | | | | 385 | | | | | 390 | | | | | 395 | | | |
| 30 | TTG | AAT | ACC | AGG | GTG | GGC | ACC | AAA | CGC | TAC | ATG | GCT | CCC | GAA | GTG | CTG | 1548 |
| | Leu | Asn | Thr | Arg | Val | Gly | Thr | Lys | Arg | Tyr | Met | Ala | Pro | Glu | Val | Leu | |
| | | | 400 | | | | | 405 | | | | | 410 | | | | |
| 35 | GAC | GAA | AGC | CTG | AAC | AAA | AAC | CAC | TTC | CAG | CCC | TAC | ATC | ATG | GCT | GAC | 1596 |
| | Asp | Glu | Ser | Leu | Asn | Lys | Asn | His | Phe | Gln | Pro | Tyr | Ile | Met | Ala | Asp | |
| | | | 415 | | | | 420 | | | | | 425 | | | | | |
| 40 | ATC | TAC | AGC | TTC | GGC | CTA | ATC | ATT | TGG | GAG | ATG | GCT | CGT | CGT | TGT | ATC | 1644 |
| | Ile | Tyr | Ser | Phe | Gly | Leu | Ile | Ile | Trp | Glu | Met | Ala | Arg | Arg | Cys | Ile | |
| | | | | | 435 | | | | | | 440 | | | | 445 | | |
| 45 | ACA | GGA | GGG | ATC | GTG | GAA | GAA | TAC | CAA | TTG | CCA | TAT | TAC | AAC | ATG | GTA | 1692 |
| | Thr | Gly | Gly | Ile | Val | Glu | Glu | Tyr | Gln | Leu | Pro | Tyr | Tyr | Asn | Met | Val | |
| | | | | 450 | | | | | | 455 | | | | | 460 | | |
| 50 | CCG | AGT | GAT | CCG | TCA | TAC | GAA | GAT | ATG | CGT | GAG | GTT | GTG | TGT | GTC | AAA | 1740 |
| | Pro | Ser | Asp | Pro | Ser | Tyr | Glu | Asp | Met | Arg | Glu | Val | Val | Cys | Val | Lys | |
| | | | | 465 | | | | | 470 | | | | | 475 | | | |
| 55 | CGT | TTG | CGG | CCA | ATT | GTG | TCT | AAT | CGG | TGG | AAC | AGT | GAT | GAA | TGT | CTA | 1788 |
| | Arg | Leu | Arg | Pro | Ile | Val | Ser | Asn | Arg | Trp | Asn | Ser | Asp | Glu | Cys | Leu | |
| | | | 480 | | | | | 485 | | | | | 490 | | | | |
| 60 | CGA | GCA | GTT | TTG | AAG | CTA | ATG | TCA | GAA | TGC | TGG | GCC | CAC | AAT | CCA | GCC | 1836 |
| | Arg | Ala | Val | Leu | Lys | Leu | Met | Ser | Glu | Cys | Trp | Ala | His | Asn | Pro | Ala | |
| | | | 495 | | | | | 500 | | | | 505 | | | | | |
| 65 | TCC | AGA | CTC | ACA | GCA | TTG | AGA | ATT | AAG | AAG | ACG | CTT | GCC | AAG | ATG | GTT | 1884 |
| | Ser | Arg | Leu | Thr | Ala | Leu | Arg | Ile | Lys | Lys | Thr | Leu | Ala | Lys | Met | Val | |
| | | | | | | 515 | | | | | 520 | | | | 525 | | |
| 70 | GAA | TCC | CAA | GAT | GTA | AAA | ATC | TGATGGTTAA | ACCATCGGAG | GAGAACTCT | | | | | | | 1935 |
| | Glu | Ser | Gln | Asp | Val | Lys | Ile | | | | | | | | | | |
| | | | | | 530 | | | | | | | | | | | | |
| 75 | AGACTGCAAG | AACTGTTTTT | ACCCATGGCA | TGGGTGGAAT | TAGAGTGGAA | TAAGGATGTT | | | | | | | | | | | 1995 |

AACTTGGTTC TCAGACTCTT TCTTCACTAC GTGTTACACAG GCTGCTAATA TTAAACCTTT 2055
 CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTCAATTCTT TATATATGGA 2115
 5 CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAAGTGCA 2175
 TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC 2235
 10 ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA 2295
 AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA 2355
 GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC 2415
 15 TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA 2475
 ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG 2535
 20 CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTAAGTTTGA 2595
 AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655
 AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTGTGG 2715
 25 TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775
 ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG 2835
 30 TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA 2895
 TATTTTGTGT ATAATGTGCT TTATTGCAA ATCACCC 2932

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 532 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr Leu Phe
 1 5 10 15
 Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly
 20 25 30
 Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu Asn Gly Val
 35 40 45
 Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser
 50 55 60
 Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly
 65 70 75 80

His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu
85 90 95

5 Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp
100 105 110

Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn
115 120 125

10 Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly
130 135 140

Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile Ser Met
145 150 155 160

15 Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr
165 170 175

Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn Arg Asp
180 185 190

20 Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp
195 200 205

25 Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
210 215 220

Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
225 230 235 240

30 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
245 250 255

Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
260 265 270

35 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
275 280 285

40 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
290 295 300

Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
305 310 315 320

45 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
325 330 335

Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
340 345 350

50 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
355 360 365

55 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
370 375 380

Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
385 390 395 400

60

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Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
405 410 415

5 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
420 425 430

Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
435 440 445

10 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
450 455 460

Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
465 470 475 480

15 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
485 490 495

20 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
500 505 510

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
515 520 525

25 Asp Val Lys Ile
530

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 187..1695
- (D) OTHER INFORMATION: /product= "Murine ALK6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGGCGGC AGAAGTTGCC GCGTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGACC 60

50 TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC 120

AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT 180

GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG 228

55 Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys
1 5 10

AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA 276

60 Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu
15 20 25 30

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| | | | | | | | | | | | | | | | | | | |
|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | CGT | TGT | AAA | TGC | CAC | CAC | CAC | TGT | CCG | GAA | GAC | TCA | GTC | AAC | AAT | ATC | 324 |
| | | Arg | Cys | Lys | Cys | His | His | His | Cys | Pro | Glu | Asp | Ser | Val | Asn | Asn | Ile | |
| | | | | | | 35 | | | | | 40 | | | | | 45 | | |
| 5 | | TGC | AGC | ACA | GAT | GGG | TAC | TGC | TTC | ACG | ATG | ATA | GAA | GAA | GAT | GAC | TCT | 372 |
| | | Cys | Ser | Thr | Asp | Gly | Tyr | Cys | Phe | Thr | Met | Ile | Glu | Glu | Asp | Asp | Ser | |
| | | | | | 50 | | | | | 55 | | | | | 60 | | | |
| 10 | | GGA | ATG | CCT | GTT | GTC | ACC | TCT | GGA | TGT | CTA | GGA | CTA | GAA | GGG | TCA | GAT | 420 |
| | | Gly | Met | Pro | Val | Val | Thr | Ser | Gly | Cys | Leu | Gly | Leu | Glu | Gly | Ser | Asp | |
| | | | | 65 | | | | | 70 | | | | | 75 | | | | |
| 15 | | TTT | CAA | TGT | CGT | GAC | ACT | CCC | ATT | CCT | CAT | CAA | AGA | AGA | TCA | ATT | GAA | 468 |
| | | Phe | Gln | Cys | Arg | Asp | Thr | Pro | Ile | Pro | His | Gln | Arg | Arg | Ser | Ile | Glu | |
| | | | 80 | | | | | 85 | | | | | 90 | | | | | |
| 20 | | TGC | TGC | ACA | GAA | AGG | AAT | GAG | TGT | AAT | AAA | GAC | CTC | CAC | CCC | ACT | CTG | 516 |
| | | Cys | Cys | Thr | Glu | Arg | Asn | Glu | Cys | Asn | Lys | Asp | Leu | His | Pro | Thr | Leu | |
| | | 95 | | | | | 100 | | | | | 105 | | | | 110 | | |
| 25 | | CCT | CCT | CTC | AAG | GAC | AGA | GAT | TTT | GTT | GAT | GGG | CCC | ATA | CAC | CAC | AAG | 564 |
| | | Pro | Pro | Leu | Lys | Asp | Arg | Asp | Phe | Val | Asp | Gly | Pro | Ile | His | His | Lys | |
| | | | | | 115 | | | | | | 120 | | | | | 125 | | |
| 30 | | GCC | TTG | CTT | ATC | TCT | GTG | ACT | GTC | TGT | AGT | TTA | CTC | TTG | GTC | CTC | ATT | 612 |
| | | Ala | Leu | Leu | Ile | Ser | Val | Thr | Val | Cys | Ser | Leu | Leu | Leu | Val | Leu | Ile | |
| | | | | | 130 | | | | | 135 | | | | | 140 | | | |
| 35 | | ATT | TTA | TTC | TGT | TAC | TTC | AGG | TAT | AAA | AGA | CAA | GAA | GCC | CGA | CCT | CGG | 660 |
| | | Ile | Leu | Phe | Cys | Tyr | Phe | Arg | Tyr | Lys | Arg | Gln | Glu | Ala | Arg | Pro | Arg | |
| | | | | 145 | | | | | 150 | | | | | 155 | | | | |
| 40 | | TAC | AGC | ATT | GGG | CTG | GAG | CAG | GAC | GAG | ACA | TAC | ATT | CCT | CCT | GGA | GAG | 708 |
| | | Tyr | Ser | Ile | Gly | Leu | Glu | Gln | Asp | Glu | Thr | Tyr | Ile | Pro | Pro | Gly | Glu | |
| | | | 160 | | | | | 165 | | | | | 170 | | | | | |
| 45 | | TCC | CTG | AGA | GAC | TTG | ATC | GAG | CAG | TCT | CAG | AGC | TCG | GGA | AGT | GGA | TCA | 756 |
| | | Ser | Leu | Arg | Asp | Leu | Ile | Glu | Gln | Ser | Gln | Ser | Ser | Gly | Ser | Gly | Ser | |
| | | 175 | | | | | 180 | | | | | 185 | | | | | 190 | |
| 50 | | GGC | CTC | CCT | CTG | CTG | GTC | CAA | AGG | ACA | ATA | GCT | AAG | CAA | ATT | CAG | ATG | 804 |
| | | Gly | Leu | Pro | Leu | Leu | Val | Gln | Arg | Thr | Ile | Ala | Lys | Gln | Ile | Gln | Met | |
| | | | | | 195 | | | | | | 200 | | | | | 205 | | |
| 55 | | GTG | AAG | CAG | ATT | GGA | AAA | GGC | CGC | TAT | GGC | GAG | GTG | TGG | ATG | GGA | AAG | 852 |
| | | Val | Lys | Gln | Ile | Gly | Lys | Gly | Arg | Tyr | Gly | Glu | Val | Trp | Met | Gly | Lys | |
| | | | | | 210 | | | | | 215 | | | | | 220 | | | |
| 60 | | TGG | CGT | GGA | GAA | AAG | GTG | GCT | GTG | AAA | GTG | TTC | TTC | ACC | ACG | GAG | GAA | 900 |
| | | Trp | Arg | Gly | Glu | Lys | Val | Ala | Val | Lys | Val | Phe | Phe | Thr | Thr | Glu | Glu | |
| | | | | 225 | | | | | 230 | | | | | 235 | | | | |
| 65 | | GCC | AGC | TGG | TTC | CGA | GAG | ACT | GAG | ATA | TAT | CAG | ACG | GTC | CTG | ATG | CGG | 948 |
| | | Ala | Ser | Trp | Phe | Arg | Glu | Thr | Glu | Ile | Tyr | Gln | Thr | Val | Leu | Met | Arg | |
| | | | 240 | | | | | 245 | | | | | 250 | | | | | |
| 70 | | CAT | GAG | AAT | ATT | CTG | GGG | TTC | ATT | GCT | GCA | GAT | ATC | AAA | GGG | ACT | GGG | 996 |
| | | His | Glu | Asn | Ile | Leu | Gly | Phe | Ile | Ala | Ala | Asp | Ile | Lys | Gly | Thr | Gly | |
| | | 255 | | | | | 260 | | | | | 265 | | | | | 270 | |

| | | | | | | | | | | | | | | | | | |
|----|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| 5 | TCC Ser | TGG Trp | ACT Thr | CAG Gln | TTG Leu 275 | TAC Tyr | CTC Leu | ATC Ile | ACA Thr | GAC Asp 280 | TAT Tyr | CAT His | GAA Glu | AAC Asn | GGC Gly 285 | TCC Ser | 1044 |
| 10 | CTT Leu | TAT Tyr | GAC Asp | TAT Tyr 290 | CTG Leu | AAA Lys | TCC Ser | ACC Thr | ACC Thr 295 | TTA Leu | GAC Asp | GCA Ala | AAG Lys | TCC Ser 300 | ATG Met | CTG Leu | 1092 |
| 15 | AAG Lys | CTA Leu | GCC Ala 305 | TAC Tyr | TCC Ser | TCT Ser | GTC Val | AGC Ser 310 | GGC Gly | CTA Leu | TGC Cys | CAT His | TTA Leu 315 | CAC His | ACG Thr | GAA Glu | 1140 |
| 20 | ATC Ile | TTT Phe 320 | AGC Ser | ACT Thr | CAA Gln | GGC Gly | AAG Lys 325 | CCA Pro | GCA Ala | ATC Ile | GCC Ala 330 | CAT His | CGA Arg | GAC Asp | TTG Leu | AAA Lys | 1188 |
| 25 | AGT Ser 335 | AAA Lys | AAC Asn | ATC Ile | CTG Leu | GTG Val 340 | AAG Lys | AAA Lys | AAT Asn | GGA Gly | ACT Thr 345 | TGC Cys | TGC Cys | ATA Ile | GCA Ala | GAC Asp 350 | 1236 |
| 30 | CTG Leu | GGC Gly | TTG Leu | GCT Ala | GTC Val 355 | AAG Lys | TTC Phe | ATT Ile | AGT Ser | GAC Asp 360 | ACA Thr | AAT Asn | GAG Glu | GTT Val | GAC Asp 365 | ATC Ile | 1284 |
| 35 | CCA Pro | CCC Pro | AAC Asn | ACC Thr 370 | CGG Arg | GTT Val | GGC Gly | ACC Thr | AAG Lys 375 | CGC Arg | TAT Tyr | ATG Met | CCT Pro | CCA Pro 380 | GAA Glu | GTG Val | 1332 |
| 40 | CTG Leu | GAC Asp | GAG Glu 385 | AGC Ser | TTG Leu | AAT Asn | AGA Arg | AAC Asn 390 | CAT His | TTC Phe | CAG Gln | TCC Ser | TAC Tyr 395 | ATT Ile | ATG Met | GCT Ala | 1380 |
| 45 | GAC Asp 400 | ATG Met | TAC Tyr | AGC Ser | TTT Phe | GGA Gly | CTC Leu 405 | ATC Ile | CTC Leu | TGG Trp | GAG Glu | ATT Ile 410 | GCA Ala | AGG Arg | AGA Arg | TGT Cys | 1428 |
| 50 | GTT Val 415 | TCT Ser | GGA Gly | GGT Gly | ATA Ile | GTG Val 420 | GAA Glu | GAA Glu | TAC Tyr | CAG Gln | CTT Leu 425 | CCC Pro | TAT Tyr | CAC His | GAC Asp | CTG Leu 430 | 1476 |
| 55 | GTG Val | CCC Pro | AGT Ser | GAC Asp | CCT Pro 435 | TCT Ser | TAT Tyr | GAG Glu | GAC Asp | ATG Met 440 | AGA Arg | GAA Glu | ATT Ile | GTG Val | TGC Cys 445 | ATG Met | 1524 |
| 60 | AAG Lys | AAG Lys | TTA Leu | CGG Arg 450 | CCT Pro | TCA Ser | TTC Phe | CCC Pro | AAT Asn 455 | CGA Arg | TGG Trp | AGC Ser | AGT Ser | GAT Asp 460 | GAG Glu | TGT Cys | 1572 |
| 65 | CTC Leu | AGG Arg | CAG Gln 465 | ATG Met | GGG Gly | AAG Lys | CTT Leu | ATG Met 470 | ACA Thr | GAG Glu | TGC Cys | TGG Trp | GCG Ala 475 | CAG Gln | AAT Asn | CCT Pro | 1620 |
| 70 | GCC Ala | TCC Ser | AGG Arg | CTG Leu | ACG Thr | GCC Ala | CTG Leu 485 | AGA Arg | GTT Val | AAG Lys | AAA Lys | ACC Thr 490 | CTT Leu | GCC Ala | AAA Lys | ATG Met | 1668 |
| 75 | TCA Ser 495 | GAG Glu | TCC Ser | CAG Gln | GAC Asp | ATT Ile 500 | AAA Lys | CTC Leu | TGACGTCAGA | TACTTGTGGA | CAGAGCAAGA | | | | | | 1722 |

ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA 1782
 GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT 1842
 5 CATGGCTTTC TGAGGAGGAG AACTGTTTG GGTAACCTGT TCAAGATATG ATGCATGTTG 1902
 CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAAAA 1952

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
 1 5 10
 25 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys
 20 25 30
 Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
 35 40 45
 30 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met
 50 55 60
 35 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
 65 70 75 80
 Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
 85 90 95
 40 Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110
 Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu
 115 120 125
 45 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140
 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser
 145 150 155 160
 50 Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175
 55 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205

60

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5 Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220
 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255
 10 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285
 15 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325 330 335
 25 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340 345 350
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365
 30 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser
 405 410 415
 40 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
 420 425 430
 Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys
 435 440 445
 45 Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
 450 455 460
 Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser
 465 470 475 480
 Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu
 485 490 495
 55 Ser Gln Asp Ile Lys Leu
 500

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10

- (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
 /product= "OP1"
 /evidence= EXPERIMENTAL
 /standard_name= "OP1"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG 57
 Met His Val
 1

25 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA 105
 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
 5 10 15

30 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC 153
 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
 20 25 30 35

35 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG 201
 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
 40

40 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC 249
 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
 55 60 65

45 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG 297
 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
 70 75 80

50 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC 345
 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
 85 90 95

55 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC 393
 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
 100 105 110 115

60 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC 441
 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
 120 125 130

55 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC 489
 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
 135 140 145

60 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC 537

0998254 101801

09022543-101801

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | His | Pro | Arg | Tyr | His | His | Arg | Glu | Phe | Arg | Phe | Asp | Leu | Ser | Lys | Ile | |
| | | | 150 | | | | | 155 | | | | | 160 | | | | |
| 5 | CCA | GAA | GGG | GAA | GCT | GTC | ACG | GCA | GCC | GAA | TTC | CGG | ATC | TAC | AAG | GAC | 585 |
| | Pro | Glu | Gly | Glu | Ala | Val | Thr | Ala | Ala | Glu | Phe | Arg | Ile | Tyr | Lys | Asp | |
| | | 165 | | | | | 170 | | | | | 175 | | | | | |
| 10 | TAC | ATC | CGG | GAA | CGC | TTC | GAC | AAT | GAG | ACG | TTC | CGG | ATC | AGC | GTT | TAT | 633 |
| | Tyr | Ile | Arg | Glu | Arg | Phe | Asp | Asn | Glu | Thr | Phe | Arg | Ile | Ser | Val | Tyr | |
| | | 180 | | | | 185 | | | | | 190 | | | | | 195 | |
| 15 | CAG | GTG | CTC | CAG | GAG | CAC | TTG | GGC | AGG | GAA | TCG | GAT | CTC | TTC | CTG | CTC | 681 |
| | Gln | Val | Leu | Gln | Glu | His | Leu | Gly | Arg | Glu | Ser | Asp | Leu | Phe | Leu | Leu | |
| | | | | | 200 | | | | | 205 | | | | | 210 | | |
| 20 | GAC | AGC | CGT | ACC | CTC | TGG | GCC | TCG | GAG | GAG | GGC | TGG | CTG | GTG | TTT | GAC | 729 |
| | Asp | Ser | Arg | Thr | Leu | Trp | Ala | Ser | Glu | Glu | Gly | Trp | Leu | Val | Phe | Asp | |
| | | | | 215 | | | | | 220 | | | | | 225 | | | |
| 25 | ATC | ACA | GCC | ACC | AGC | AAC | CAC | TGG | GTG | GTC | AAT | CCG | CGG | CAC | AAC | CTG | 777 |
| | Ile | Thr | Ala | Thr | Ser | Asn | His | Trp | Val | Val | Asn | Pro | Arg | His | Asn | Leu | |
| | | | 230 | | | | | 235 | | | | | 240 | | | | |
| 30 | GGC | CTG | CAG | CTC | TCG | GTG | GAG | ACG | CTG | GAT | GGG | CAG | AGC | ATC | AAC | CCC | 825 |
| | Gly | Leu | Gln | Leu | Ser | Val | Glu | Thr | Leu | Asp | Gly | Gln | Ser | Ile | Asn | Pro | |
| | | 245 | | | | | 250 | | | | | 255 | | | | | |
| 35 | AAG | TTG | GCG | GGC | CTG | ATT | GGG | CGG | CAC | GGG | CCC | CAG | AAC | AAG | CAG | CCC | 873 |
| | Lys | Leu | Ala | Gly | Leu | Ile | Gly | Arg | His | Gly | Pro | Gln | Asn | Lys | Gln | Pro | |
| | | 260 | | | | 265 | | | | | 270 | | | | | 275 | |
| 40 | TTC | ATG | GTG | GCT | TTC | TTC | AAG | GCC | ACG | GAG | GTC | CAC | TTC | CGC | AGC | ATC | 921 |
| | Phe | Met | Val | Ala | Phe | Lys | Lys | Ala | Thr | Glu | Val | His | Phe | Arg | Ser | Ile | |
| | | | | | 280 | | | | | 285 | | | | | 290 | | |
| 45 | CGG | TCC | ACG | GGG | AGC | AAA | CAG | CGC | AGC | CAG | AAC | CGC | TCC | AAG | ACG | CCC | 969 |
| | Arg | Ser | Thr | Gly | Ser | Lys | Gln | Arg | Ser | Gln | Asn | Arg | Ser | Lys | Thr | Pro | |
| | | | | 295 | | | | | 300 | | | | | 305 | | | |
| 50 | AAG | AAC | CAG | GAA | GCC | CTG | CGG | ATG | GCC | AAC | GTG | GCA | GAG | AAC | AGC | AGC | 1017 |
| | Lys | Asn | Gln | Glu | Ala | Leu | Arg | Met | Ala | Asn | Val | Ala | Glu | Asn | Ser | Ser | |
| | | | 310 | | | | | 315 | | | | | 320 | | | | |
| 55 | AGC | GAC | CAG | AGG | CAG | GCC | TGT | AAG | AAG | CAC | GAG | CTG | TAT | GTC | AGC | TTC | 1065 |
| | Ser | Asp | Gln | Arg | Gln | Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr | Val | Ser | Phe | |
| | | 325 | | | | | 330 | | | | | 335 | | | | | |
| 60 | CGA | GAC | CTG | GGC | TGG | CAG | GAC | TGG | ATC | ATC | GCG | CCT | GAA | GGC | TAC | GCC | 1113 |
| | Arg | Asp | Leu | Gly | Trp | Gln | Asp | Trp | Ile | Ile | Ala | Pro | Glu | Gly | Tyr | Ala | |
| | | 340 | | | | 345 | | | | | 350 | | | | | 355 | |
| 65 | GCC | TAC | TAC | TGT | GAG | GGG | GAG | TGT | GCC | TTC | CCT | CTG | AAC | TCC | TAC | ATG | 1161 |
| | Ala | Tyr | Tyr | Cys | Glu | Gly | Glu | Cys | Ala | Phe | Pro | Leu | Asn | Ser | Tyr | Met | |
| | | | | | 360 | | | | | 365 | | | | | 370 | | |
| 70 | AAC | GCC | ACC | AAC | CAC | GCC | ATC | GTG | CAG | ACG | CTG | GTC | CAC | TTC | ATC | AAC | 1209 |
| | Asn | Ala | Thr | Asn | His | Ala | Ile | Val | Gln | Thr | Leu | Val | His | Phe | Ile | Asn | |
| | | | | 375 | | | | | 380 | | | | | 385 | | | |
| 75 | CCG | GAA | ACG | GTG | CCC | AAG | CCC | TGC | TGT | GCG | CCC | ACG | CAG | CTC | AAT | GCC | 1257 |

(2) INFORMATION FOR SEQ ID NO:10:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30
45 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45
50 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80
55 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110

60

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30
45 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45
50 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
55 60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80
55 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110

09854-101801

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125

5 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

10 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

15 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205

20 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

25 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270

30 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
275 280 285

35 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305 310 315 320

40 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
340 345 350

45 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
370 375 380

50 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385 390 395 400

55 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
420 425 430

60

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..102

(D) OTHER INFORMATION: /label= OPX
 /note= "Each Xaa is independently selected from
 a group of one or more specified amino acids
 as defined in the specification"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Xaa | Xaa | His | Glu | Leu | Tyr | Val | Xaa | Phe | Xaa | Asp | Leu | Gly | Trp | Xaa |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | Trp | Xaa | Ile | Ala | Pro | Xaa | Gly | Tyr | Xaa | Ala | Tyr | Tyr | Cys | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Cys | Xaa | Phe | Pro | Leu | Xaa | Ser | Xaa | Met | Asn | Ala | Thr | Asn | His | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Xaa | Gln | Xaa | Leu | Val | His | Xaa | Xaa | Xaa | Pro | Xaa | Xaa | Val | Pro | Lys |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Xaa | Cys | Cys | Ala | Pro | Thr | Xaa | Leu | Xaa | Ala | Xaa | Ser | Val | Leu | Tyr | Xaa |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asp | Xaa | Ser | Xaa | Asn | Val | Xaa | Leu | Xaa | Lys | Xaa | Arg | Asn | Met | Val | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Xaa | Ala | Cys | Gly | Cys | His | | | | | | | | | | |
| | | | | | 100 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGGATCCTG TTGTGAAGGN AATATGTG

28

(2) INFORMATION FOR SEQ ID NO:13:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

35 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO:15:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

55 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60 CGGAATTCTG GTGCCATATA

20

FOR "CH22660"